

# Constructing supertrees: an example using RadCon

## *Principles*

Supertree methods belong to a growing field of phylogenetic research. The problem to be solved by these methods can be formulated as follows: Provided several trees are given that only partially contain the same terminal taxa, find the single tree or consensus that represents the information contained in all single trees in the best way. Here, we only introduce the supertree method called Matrix Representation Using Parsimony (MRP) as implemented in RadCon (Thorley and Page 2000).

## *Requirements*

You need at least two datasets with partially overlapping taxon composition. As far as taxa overlap, the taxon labels should be identical in both datasets. For comparison purposes, a combined dataset (lacking sequence information coded as ?'s) would be useful.

## *Procedure*

- Execute and analyse your first dataset in PAUP\*. You may use your favourite tree-building method.
- Save trees in NEXUS format without translation table and branch lengths:  
`savetrees format=altnexus brlens=no file=dataset1.tre replace;`
- Execute and analyse your second dataset in PAUP\*. Preferentially, use the same tree-building method as for the first dataset.
- Save trees in NEXUS format without translation table and branch lengths:  
`savetrees format=altnexus brlens=no file=dataset2.tre replace;`
- Open the program RadCon (located in your phylogeny course software folder).
- Use the File...open... menu option to open dataset1.tre with RadCon.
- Use the source...add trees... menu option to read in dataset2.tre, too.
- Use the source...Supertree consensus...MRP menu option to write a MRP matrix in Component Coding. (If necessary, deroot the trees first.) Save the corresponding matrix in a new file mymrp.nex.
- Execute mymrp.nex with PAUP\* and construct most parsimonious trees and the strict consensus of these under appropriate heuristic search options.
- If available, analyse the combined dataset with the same tree-building method as the two separate datasets.

## *Questions*

- Have a look at the MRP NEXUS file produced by RadCon. What is the meaning of the 0's and 1's in the data block?
- How does the MRP method cope with the fact that taxon sets are usually non-overlapping if supertrees are to be constructed?
- Are there differences between the supertree and the tree constructed from the combined dataset?
- You have heard that Maximum Parsimony may be inconsistent under some conditions. Is the construction of trees from MRP matrices with Parsimony affected by these findings?
- Could a supertree method also make sense if taxon sets completely overlap?